

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 14:21:24 ; Search time 126 Seconds

(without alignments)
7557,903 Million cell updates/sec

Title: US-09-943-075A-1_COPY_115_1830

Perfect score: 1716

Sequence: 1 atggaagatctctcgcggggc.....aggacaagccatgatgctc 1716

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

1: Issued Patents NA.*
2: /cgn2_6/prodata/2/ina/5A COMB.seq.*
3: /cgn2_6/prodata/2/ina/5B COMB.seq.*
4: /cgn2_6/prodata/2/ina/5C COMB.seq.*
5: /cgn2_6/prodata/2/ina/5D COMB.seq.*
6: /cgn2_6/prodata/2/ina/5E COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1512	88.1	2303	4	US-09-197-970B-4
2	79	4.6	190	1	US-09-985-799-95
3	79	4.6	190	1	US-08-594-031-95
4	79	4.6	217	1	US-09-985-799-112
5	79	4.6	217	1	US-08-594-031-112
6	79	4.6	223	1	US-09-985-799-116
7	79	4.6	223	1	US-08-594-031-116
8	79	4.6	260	1	US-09-985-799-119
9	79	4.6	260	1	US-08-594-031-119
10	79	4.6	262	1	US-09-985-799-93
11	79	4.6	262	1	US-08-594-031-93
12	79	4.6	286	1	US-09-985-799-121
13	79	4.6	286	1	US-08-594-031-121
14	79	4.6	335	1	US-09-985-799-92
15	79	4.6	335	1	US-09-985-799-96
16	79	4.6	335	1	US-09-985-799-96
17	79	4.6	335	1	US-09-985-799-123
18	79	4.6	335	1	US-08-594-031-92
19	79	4.6	335	1	US-08-594-031-94
20	79	4.6	335	1	US-08-594-031-96
21	79	4.6	473	1	US-08-594-031-123
22	79	4.6	473	1	US-09-985-799-115
23	79	4.6	473	1	US-08-594-031-115
24	79	4.6	620	1	US-09-985-799-113
25	79	4.6	620	1	US-08-594-031-113
26	79	4.6	2213	3	US-09-383-586-27
27	59	3.4	335	1	US-09-985-799-111

28	59	3.4	335	1	US-08-594-031-111	Sequence 111, App
29	59	3.4	354	1	US-09-985-799-114	Sequence 114, App
30	59	3.4	354	1	US-08-594-031-114	Sequence 114, App
31	41	2.4	292	1	US-09-985-799-107	Sequence 107, App
32	41	2.4	292	1	US-08-594-031-107	Sequence 107, App
33	41	2.4	524	1	US-09-985-799-105	Sequence 105, App
34	41	2.4	524	1	US-08-594-031-105	Sequence 105, App
35	38	2.2	240	1	US-09-985-799-118	Sequence 118, App
36	38	2.2	240	1	US-08-594-031-118	Sequence 118, App
37	33	1.9	2669	1	US-09-985-799-91	Sequence 91, App1
38	33	1.9	2669	1	US-08-594-031-91	Sequence 91, App1
39	33	1.9	2669	1	US-08-594-031-91	Sequence 91, App1
40	33	1.9	2669	1	US-08-594-031-101	Sequence 101, App
41	27	1.6	224	1	US-09-985-799-122	Sequence 122, App
42	27	1.6	224	1	US-08-594-031-122	Sequence 122, App
43	27	1.6	231	1	US-09-985-799-120	Sequence 120, App
44	27	1.6	231	1	US-08-594-031-120	Sequence 120, App
45	27	1.6	247	1	US-09-985-799-117	Sequence 117, App

ALIGNMENTS

RESULT 1
US-09-197-970B-4
Sequence 4, Application US/09197970B
Patent No. 6664385
GENERAL INFORMATION:
APPLICANT: Michele Sanicola-Nadel
Joseph V. Bonventre
Catherine A. Heeslon
Takaharu Ichimura
Henry Wei
Richard L. Cate
TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09197,970B
FILING DATE: 23-May-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,228
FILING DATE: 24-May-1996
ATTORNEY/AGENT INFORMATION:
NAME: Levine, Leslie M.
REGISTRATION NUMBER: 35,245
REFERENCE/DOCKET NUMBER: A010 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 679-2810
TELEFAX: (617) 679-2838
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..1822
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
US-09-985-799-95
SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Query Match 4.6%; Score 79; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTCTCTCAAGTGAAGTTGGGGACAACACTGGCTGTTGTCTCCACA 886
DB 181 ACTGCGCATTCTCTCAAGTGAAGTTGGGGACAACACTGGCTGTTGTCTCCACA 122
QY 887 ATCACACTTGAATCACAC 905
DB 121 ATCACACTTGAATCACAC 103

RESULT 3
US-08-594-031-95/c
Sequence 95, Application US/08594031
Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-95

Query Match 4.6%; Score 79; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTCTCTCAAGTGAAGTTGGGGACAACACTGGCTGTTGTCTCCACA 886
DB 181 ACTGCGCATTCTCTCAAGTGAAGTTGGGGACAACACTGGCTGTTGTCTCCACA 122
QY 887 ATCACACTTGAATCACAC 905
DB 121 ATCACACTTGAATCACAC 103

RESULT 4
US-09-985-799-112
Sequence 112, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

```

?      HYPOTHEITICAL: NO
?      ANTI-SENSE: NO
?      FRAGMENT TYPE: <Unknown>
?      ORIGINAL SOURCE:
?      SEQUENCE DESCRIPTION: SEQ ID NO: 112
US-09-985-799-112

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Query Match      4.6%; Score 79; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Dy 827 ACTCTGCATTTCCTACAGTGAACCTTTGGGACAACACTGCCCTGTGTGTCCACAA 88
| | | | |
Db 9 ACTCTGCATTTCCTACAGTGAACCTTTGGGACAACACTGCCCTGTGTGTCCACAA 68

QY 887 ATCACACTTTGAATCACAC 905
|||
Db 69 ATCACACTTTGAATCACAC 87

RESULT 5

US-08-594-031-112
; Sequence 112, Application US/08594031
; Patent No. 5783182

GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
INVENTOR: THOMPSON, Timothy C.

NUMBER OF SEQUENCES: 1/5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400

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; ; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/
 ; FILING DATE: 30-JAN-199
 ; CLASSIFICATION: 435
 ; PRIORITY DATE:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/006,838
 ; FILING DATE: 16-NOV-1995
 ; ATTORNEY/AGENT INFORMATION:

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890

TELEX: INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:

LENGTH: 217 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
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US-08-594-031-112

Query Match 4.6%; Score 79; DB 1; Length 217;

Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0

827 ACTCTGCCATTTCCTACACAGTGGAACTTTGGGGACACACACTGGCCTGTTGTCTCCAACA 886

Db 9 ACTGCGATTTCTTACAAGTGAAGCTTTGGGGAACAACCTGGCTGTTGTCTCAACA 60
 Qy 887 ATCAACCTTGAATCAAC 905
 Db 69 ATCAACCTTGAATCAAC 87

RESULT 6
US-09-985-799-116/c

```

; Patent No. RE38392
;
; GENERAL INFORMATION:
;
; APPLICANT: THOMPSON, Timothy C.
;
; TITLE OF INVENTION: METHOD FOR DETERMINING MEAN-LENGTH SEQUENCES

```

NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
ADDRESS: 1000 Pennsylvania Avenue, N.W.
Washington, D.C. 20004-4242
TELEPHONE: (202) 691-8000
FACSIMILE: (202) 691-8001
ELECTRONIC MAIL: BAKER@BBT.COM

—

COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; FORMATTED BY: Photo View
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SOFTWARE: FASTCSD VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NO. RE38392-2001

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; CLASSIFICATION: <UNKNOWN>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
;

```

APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110

TELECOMMUNICATION INFORMATION
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
E-MAIL: Telnet@...

```

;      LENGTH: 223 base pairs
;      INFORMATION FOR SEQ ID NO: 116:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 223 base pairs

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LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

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; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SE
;

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US-09-985-799-116

Query Match 4.6%; Score 79; L

Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0
Gaps 0

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Oy      827 ACCTCGCATTTTCTACAGTGGAACTTTGGGGAACAACAATGGCTGTGTCTCCACA 886
        |||||
Db      178 ACTTCGCATTTCCTACAAGTGGAACTTTGGGGAACAACAATGGCTGTGTCTCCACA 119
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887 ATCACACTTGAATCACAC 905

Db 118 ATCACAATTGATCACC 100

RESULT 7

US-08-594-031-116/C
; Sequence 116, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-594-031-116
Query Match 4.6%; Score 79; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 827 ACTGTGCAATTCCTCAAGTGAACCTTTGGGACAACTGGCTGTGTCTCCACA 886
DB 178 ACTGTGCAATTCCTCAAGTGAACCTTTGGGACAACTGGCTGTGTCTCCACA 119
QY 887 ATCACACTTGAATCACAC 905
DB 118 ATCACACTTGAATCACAC 100

RESULT 8
US-09-985-799-119/C
; Sequence 119, Application US/09985799
; Patent No. RE38392
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC

COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 119:
US-09-985-799-119
Query Match 4.6%; Score 79; DB 1; Length 260;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 827 ACTGTGCAATTCCTCAAGTGAACCTTTGGGACAACTGGCTGTGTCTCCACA 886
DB 178 ACTGTGCAATTCCTCAAGTGAACCTTTGGGACAACTGGCTGTGTCTCCACA 119
QY 887 ATCACACTTGAATCACAC 905
DB 118 ATCACACTTGAATCACAC 100

RESULT 9
US-08-594-031-119/C
; Sequence 119, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031

FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-09-943-031-119

Query Match 4.6%; Score 79; DB 1; Length 260;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTTCTCAAGTGGAACTTTGGGACACACTGGCCTGTTGTCTCCAA 886
DB 178 ACTGCGCATTTCTCAAGTGGAACTTTGGGACACACTGGCCTGTTGTCTCCAA 119
QY 887 ATCACACTTTGATCACAC 905
DB 118 ATCACACTTTGATCACAC 100

RESULT 10
US-09-985-799-93
Sequence 93, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-985-799-93

Query Match 4.6%; Score 79; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTTCTCAAGTGGAACTTTGGGACACACTGGCCTGTTGTCTCCAA 886
DB 155 ACTGCGCATTTCTCAAGTGGAACTTTGGGACACACTGGCCTGTTGTCTCCAA 214
QY 887 ATCACACTTTGATCACAC 905
DB 215 ATCACACTTTGATCACAC 233

RESULT 11
US-09-943-031-93
Sequence 93, Application US/08594031
Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:

Query Match
Best Local Similarity 4.6%; Score 79; DB 1; Length 262;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGGCCCTGTTGTCTCCACA 886
DB 155 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGGCCCTGTTGTCTCCACA 214
QY 887 ATCACACTTTGAATCACAC 905
DB 215 ATCACACTTTGAATCACAC 233

RESULT 12

US-09-985-799-121/c
Sequence 121, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
US-09-985-799-121

Query Match
Best Local Similarity 4.6%; Score 79; DB 1; Length 286;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGGCCCTGTTGTCTCCACA 886
DB 153 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGGCCCTGTTGTCTCCACA 94
QY 887 ATCACACTTTGAATCACAC 905
DB 93 ATCACACTTTGAATCACAC 75

RESULT 13

US-08-594-031-121/c
Sequence 121, Application US/08594031
Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-121

Query Match
Best Local Similarity 4.6%; Score 79; DB 1; Length 286;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGGCCCTGTTGTCTCCACA 886
DB 153 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGGCCCTGTTGTCTCCACA 94
QY 887 ATCACACTTTGAATCACAC 905
DB 93 ATCACACTTTGAATCACAC 75

RESULT 14
US-09-985-799-92
Sequence 92, Application US/09985799

Patent No. RE38392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-09-985-799-92
Query Match 4.6%; Score 79; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 827 ACTGCGCATTTCTTCAAGTGAAGTGGGAGCAACACTGCGCTGTTGTCTCCACA 886
DB 155 ACTGCGCATTTCTTCAAGTGAAGTGGGAGCAACACTGCGCTGTTGTCTCCACA 214
QY 887 ATCACACTTTGATCACAC 905
DB 215 ATCACACTTTGATCACAC 233
RESULT 15
US-09-985-799-94
Sequence 94, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-985-799-94
Query Match 4.6%; Score 79; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 5.1e-30;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 827 ACTGCGCATTTCTTCAAGTGAAGTGGGAGCAACACTGCGCTGTTGTCTCCACA 886
DB 155 ACTGCGCATTTCTTCAAGTGAAGTGGGAGCAACACTGCGCTGTTGTCTCCACA 214
QY 887 ATCACACTTTGATCACAC 905
DB 215 ATCACACTTTGATCACAC 233
Search completed: April 30, 2004, 16:17:56
Job time: 126 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 16:08:04 ; Search time 711 Seconds

(without alignments)
10917.390 Million cells updates/sec

Title: US-09-943-075A-1_COPY_115_1830

Perfect score: 1716
Sequence: 1 atggaagctctctcgaggtc.....aggacacgcctgagctctc 1716

Scoring table: OLIGO_NTC

Gapop 60.0 , Gapext 60.0

Searched: 2936184 seqs, 2261732022 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1716	100.0	2320 9 US-09-943-075A-1	Sequence 1, Appl1
2	425	24.8	631 17 US-10-404-460-119	Sequence 129, App
3	178	10.4	294 9 US-09-917-800A-119	Sequence 139, App
4	178	10.4	294 12 US-10-152-319A-122	Sequence 132, App
5	178	10.4	294 16 US-10-191-803-372	Sequence 372, App
6	79	4.6	1725 9 US-09-943-075A-7	Sequence 7, Appl1
7	79	4.6	2213 9 US-09-823-038A-27	Sequence 27, Appl1
8	65	3.8	65 10 US-09-908-975-1458	Sequence 1458, Ap
9	33	1.9	318 9 US-09-864-761-18279	Sequence 18279, A
10	33	1.9	478 9 US-09-864-761-15279	Sequence 15279, Ap
11	33	1.9	1393 17 US-10-309-290-153	Sequence 153, App
12	33	1.9	1410 17 US-10-309-290-149	Sequence 149, App
13	33	1.9	1542 17 US-10-309-290-147	Sequence 147, App
14	33	1.9	1683 9 US-09-943-075A-8	Sequence 8, Appl1

15	33	1.9	1923 17 US-10-309-290-151	Sequence 151, App
16	33	1.9	2661 13 US-10-463-106-1	Sequence 1, Appl1
17	33	1.9	2661 14 US-10-039-272-1	Sequence 1, Appl1
18	33	1.9	2666 15 US-10-084-817-169	Sequence 169, App
19	33	1.9	2669 10 US-09-525-978B-82	Sequence 82, App
20	33	1.9	2669 13 US-10-342-887-779	Sequence 779, App
21	33	1.9	2669 13 US-10-172-118-779	Sequence 779, App
22	33	1.9	2669 16 US-10-295-027-1041	Sequence 1041, Ap
23	33	1.9	2683 13 US-10-219-535-41	Sequence 41, Appl
24	33	1.9	2683 13 US-10-232-230-41	Sequence 41, Appl
25	33	1.9	2683 13 US-10-232-224-41	Sequence 41, Appl
26	33	1.9	2683 15 US-10-227-884-41	Sequence 41, Appl
27	33	1.9	2683 15 US-10-230-163-41	Sequence 41, Appl
28	33	1.9	2683 15 US-10-230-338-41	Sequence 41, Appl
29	33	1.9	2683 15 US-10-218-631-41	Sequence 41, Appl
30	33	1.9	2683 15 US-10-230-414-41	Sequence 41, Appl
31	33	1.9	2683 15 US-10-216-159A-41	Sequence 41, Appl
32	33	1.9	2683 15 US-10-218-849-41	Sequence 41, Appl
33	33	1.9	2683 15 US-10-227-873-41	Sequence 41, Appl
34	33	1.9	2683 15 US-10-227-883-41	Sequence 41, Appl
35	33	1.9	2683 15 US-10-219-076-41	Sequence 41, Appl
36	33	1.9	2683 15 US-10-230-434-41	Sequence 41, Appl
37	33	1.9	2683 15 US-10-219-003-41	Sequence 41, Appl
38	33	1.9	2683 15 US-10-219-075-41	Sequence 41, Appl
39	33	1.9	2683 15 US-10-219-464-41	Sequence 41, Appl
40	33	1.9	2683 15 US-10-219-479-41	Sequence 41, Appl
41	33	1.9	2683 15 US-10-219-481-41	Sequence 41, Appl
42	33	1.9	2683 15 US-10-230-260-41	Sequence 41, Appl
43	33	1.9	2683 15 US-10-232-231-41	Sequence 41, Appl
44	33	1.9	2683 15 US-10-232-233-41	Sequence 41, Appl
45	33	1.9	2683 15 US-10-232-233-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-943-075A-1
Sequence 1, Application US/09943075A
Patent No. US2002015148A1
GENERAL INFORMATION:
APPLICANT: Popoff, Steven N.
APPLICANT: Safado, Favez F.
APPLICANT: Owen, Thomas A.
TITLE OF INVENTION: Osteocalcin Protein and Nucleic Acids Encoding the Same,
FILE REFERENCE: 71369, 262
CURRENT APPLICATION NUMBER: US/09/943, 075A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/229, 006
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2320
TYPE: DNA
ORGANISM: Rat osteocalcin
FEATURE:
NAME/KEY: CDS
LOCATION: (115)...(1833)
US-09-943-075A-1

Query Match 100.0%; Score 1716; DB 9; Length 2320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAGCTCTCTCGAGGTCTCGATTCTGCTGCTGACAGACTGCGCTCCAG 60
DB 115 ATGGAAGCTCTCTCGAGGTCTCGATTCTGCTGCTGACAGACTGCGCTCCAG 174
QY 61 GCGGCCAACCGGTCCTGATGCTGCTGCGCATGACGATTCACGATGACGAGGAG 120

Db 175 GGGGCGAAGCGGTTCCGATGATGCTGGGCGCATGAGCAGTATCCGGAATCATGAGGAG 234
Qy 121 AACACCAATTAAGTGGCTGTCTTCAAGATGAATGAATGAGATGAACAGCTGTATCCA 180
Db 235 AACACCAATTAAGTGGCTGTCTTCAAGATGAATGAATGAGATGAACAGCTGTATCCA 294
Qy 181 GTGTGAG 240
Db 295 GTGTGAG 354
Qy 241 GGCCTAACCATGATTCACCGGCTTGGTGGGTTCCAAATATCACTTCGTAGTAACTCG 300
Db 355 GGCCTAACCATGATTCACCGGCTTGGTGGGTTCCAAATATCACTTCGTAGTAACTCG 414
Qy 301 GTGTTCCTCCAGATGCGAAGAGAGATGCGAAGATATGCTGTATGAGAGAGATGCG 360
Db 415 GTGTTCCTCCAGATGCGAAGAGAGATGCGAAGATATGCTGTATGAGAGAGATGCG 474
Qy 361 AGAAGTGAATTTGAGAGCTGGCTTGTGACCCGATATGCTCACTGAGACACAGAGGAGAG 420
Db 475 AGAAGTGAATTTGAGAGCTGGCTTGTGACCCGATATGCTCACTGAGACACAGAGGAGAG 534
Qy 421 GATGAGAGCTGGAGAGCAACACAGCCAGAGGCGACAGCTCAGGTTCCCGAGCGAGAG 480
Db 535 GATGAGAGCTGGAGAGCAACACAGCCAGAGGCGACAGCTCAGGTTCCCGAGCGAGAG 594
Qy 481 CCTTCCCTCGCCCGCCAG 540
Db 595 CCTTCCCTCGCCCGCCAG 654
Qy 541 GGTCAGTATTTTCAAAAGCTGGGTGAGTTCAGACAGAGTTTCTATTAACAGAGTCAAC 600
Db 655 GGTCAGTATTTTCAAAAGCTGGGTGAGTTCAGACAGAGTTTCTATTAACAGAGTCAAC 714
Qy 601 TTGACAGTGGCCCTCAGGTGATGAGAGATGTTGTCTTTCGAGAGACAGGCGCGAGTAC 660
Db 715 TTGACAGTGGCCCTCAGGTGATGAGAGATGTTGTCTTTCGAGAGACAGGCGCGAGTAC 774
Qy 661 ATTTCCATCTCCAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 775 ATTTCCATCTCCAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834
Qy 721 ACCATGTACAGAGAGATGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 835 ACCATGTACAGAGAGATGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 894
Qy 781 ATTTCTTCATGATGCTCATTCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCC 840
Db 895 ATTTCTTCATGATGCTCATTCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCC 954
Qy 841 TACAGATGGAATTTGGGAGCAACAGCTGGCTGTGTGTCTTCACAAATCACTCTTGAT 900
Db 955 TACAGATGGAATTTGGGAGCAACAGCTGGCTGTGTGTCTTCACAAATCACTCTTGAT 1014
Qy 901 CACAGTATGCTCAATGGAACCTTCACTTAACTCACTCACTCACTCACTCACTCACTCACT 960
Db 1015 CACAGTATGCTCAATGGAACCTTCACTTAACTCACTCACTCACTCACTCACTCACTCACT 1074
Qy 961 GAACCATGCCCCCAACCAACCTTGGCTTCTTTCGATCTTCTTGGCTGATCTT 1020
Db 1075 GAACCATGCCCCCAACCAACCTTGGCTTCTTTCGATCTTCTTGGCTGATCTT 1134
Qy 1021 TCGGCTTCAACCACTTATGACAGCTAGTCCCTTATGAGCTCACTGAGTCAAAATCC 1080
Db 1135 TCGGCTTCAACCACTTATGACAGCTAGTCCCTTATGAGCTCACTGAGTCAAAATCC 1194
Qy 1081 ATGAGCTGAGTGAATTTCCATGATGAATGCGAGATGAACAGATATGTTACTTCA 1140
Db 1195 ATGAGCTGAGTGAATTTCCATGATGAATGCGAGATGAACAGATATGTTACTTCA 1254
Qy 1141 GCCACCATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
Db 1255 GCCACCATCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1314

Qy 1201 CCATTTCCCAACATGCAAGCTGATGAACTCACTGATGAACTTCACTTGTGACCTGAAAGG 1260
Db 1315 CCATTTCCCAACATGCAAGCTGATGAACTCACTGATGAACTTCACTTGTGACCTGAAAGG 1374
Qy 1261 GCCATCCCAAGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1375 GCCATCCCAAGAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1434
Qy 1321 AGGATGTGACCCCGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1435 AGGATGTGACCCCGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1494
Qy 1381 AATGGTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1495 AATGGTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1554
Qy 1441 ACCAGGCGCTGATCTGTATCCCTGGCAAGAGCTAGGCTCCCTCTGAGAGAGATGAT 1500
Db 1555 ACCAGGCGCTGATCTGTATCCCTGGCAAGAGCTAGGCTCCCTCTGAGAGAGATGAT 1614
Qy 1501 GGTGTCTGATCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Db 1615 GGTGTCTGATCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1674
Qy 1561 TACAAAAACACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1675 TACAAAAACACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1734
Qy 1621 AAAAGCTGAGTGTGTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1735 AAAAGCTGAGTGTGTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1794
Qy 1681 AAGATCCATCTGCTCCAGAGCAAGGCAATGATGCTC 1716
Db 1795 AAGATCCATCTGCTCCAGAGCAAGGCAATGATGCTC 1830

RESULT 2

US-10-404-460-129
; Sequence 129, Application US/10404460
; Publication No. US20040076974A1
; GENERAL INFORMATION:
; APPLICANT: PHASE-1 Molecular Toxicology, Inc.
; APPLICANT: Kier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Usna
; TITLE OF INVENTION: Liver Necrosis Predictive Genes
; FILE REFERENCE: 2874-022
; CURRENT APPLICATION NUMBER: US/10/404,460
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/369,287
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: predictive genes for liver necrosis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2, 589, 626
; OTHER INFORMATION: n = A,T,C or G
; US-10-404-460-129

Query Match

24.8%; Score 425; DB 17; Length 631;
Best Local Similarity 100.0%; Pred. No. 5.9e-214;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAAGTCTCGCGGGGTCGTGATTTCTGCTGCTGAGAGAGTCCGCTCCAG 60

Db	163	ATGGAAAGTCTGTGGGGGTCCTGGATTTCGTGCTGGTCGACAGGACTGCCGCTCCAG	2222
Qy	61	GCGGCCAAACGGTTCCTGTATGTGCTGGGCCATGACAGTATCGGATTCACATGAGGAG	1200
	223	GCGGCCAAACGGTTCCTGTGATGTGCTGGGCCATGACAGTATCCGATTCACATGAGGAG	2828
Qy	121	AACACCAATTACGTGGCTGGTCTTCACATGAAAAATGAAATGGGATGAAACGCTGATCCA	1800
Db	283	AACACCAATTACGTGGCTGGTCTTCACATGAAAAATGAAATGGGATGAAACGCTGATCCA	3420
Qy	181	GTGGAGGAGAGGAGAGAGGACAGATGAAAGGACTCTGGAGAGAGAGGCGGTGGACAGCA	2400
Db	343	GTGGAGGAGAGGAGAGAGGACAGATGAAAGGACTCTGGAGAGAGAGGCGGTGGACAGCA	4020
Qy	241	GCCCTAACAGATGATTCACCGAGCTTGGTGGATTCCAAATATCACCCTTCGTAGTGAACCTG	3000
Db	403	GCCCTAACAGATGATTCACCGAGCTTGGTGGATTCCAAATATCACCCTTCGTAGTGAACCTG	4620
Qy	301	GTGTTCGCCAGATGCCAGAAAGAAATGCCAACGGCAATATGTCATATGAGAGAACTGC	3600
Db	463	GTGTTCGCCAGATGCCAGAAAGAAATGCCAACGGCAATATGTCATATGAGAGAACTGC	5220
Qy	361	AGAAAGTATTTGAGACTTGCTTCTGACCCGATATGTCTACATCTGAGCCAAGGGGCGAGAC	4200
Db	523	AGAAAGTATTTGAGACTTGCTTCTGACCCGATATGTCTACATCTGAGCCAAGGGGCGAGAC	5820
Qy	421	GATGA 425	
Db	583	GATGA 587	

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Query Match	10.4%	Score 178	DB 9	Length 294
Best Local Similarity	100.0%	Prod. No. 3.4e-83		
Matches 178	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1075	AAATCCATGAGCGCTAGTGACATTTCCAAATGATAAACTCCGATATAAACAGATATGCTTAC	1134	
Db	294	AAATCCATGAGCGCTAGTGACATTTCCAAATGATAAACTCCGATATTAACAGATATGCTTAC	235	
QY	1135	TTGAGGCGCCACCATGACATTTGTAGATGGAACTCTTAAGATCAACTATCTCCAGGTGCA	1199	
Db	234	TTGAGGCGCCACCATGACATTTGTAGATGGAACTCTTAAGATCAACTATCTCCAGGTGCA	175	
QY	1195	GATGTCCCAATCCCACTAGCGAGCTGGAACATCTCATGATGACCTTCACTGTGACCT	1252	
Db	174	GATGTCCCAATCCCACTAGCGAGCTGGAACATCTCATGATGACCTTCACTGTGACCT	117	

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RESULT 4
US-10-152-319A-122/c
; Sequence 122, Application US/10155319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Casle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 122
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AA851814
US-10-152-319A-122

Query Match      10.4%; Score 178; DB 12; Length 294;
Best Local Similarity 100.0%; Pred. No. 3,4e-83;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1075 AAATCGTAGGAGCTAGAGCATTTCCATTAATAAACTGGCGGATTAACAGATATGCTTAC 113
294 AAATCGTAGGAGCTAGAGCATTTCCATTAATAAACTGGCGGATTAACAGATATGCTTAC 225

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QY	1135	TTGAGGACCAATCTAGATGGAATCTGGAAGCAACATCATCAGGTGCA	1194
DQ	234	TTGAGGACCAATCTAGATGGAATCTGGAAGCAACATCATCAGGTGCA	175
QY	1135	GATGTCCCAATGCCAATGAGCGCTGCAATCTCAATGAGCATCTTATGACCT	1232
DQ	174	GATGTCCCAATGCCAATGAGCGCTGCAATCTCAATGAGCATCTTATGACCT	117

RESULT 5

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US-10-191-803-372/c
/ Sequence 372, Application US/10191803
/ Publication No. US20040014040A1
/ GENERAL INFORMATION:
/ APPLICANT: MENDRICK, Donna
/ APPLICANT: PORTER, Mark
/ APPLICANT: JOHNSON, Kory
/ APPLICANT: HIGGS, Brandon
/ APPLICANT: CASTLE, Arthur
/ APPLICANT: ELASHOFF, Michael
/ TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
/ FILE REFERENCE: 44921-5090US
/ CURRENT APPLICATION NUMBER: US/10/191,803
/ PRIOR FILING DATE: 2002-07-10
/ PRIOR APPLICATION NUMBER: US 60/303,819
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/305,623
/ PRIOR FILING DATE: 2001-07-17
/ PRIOR APPLICATION NUMBER: US 60/369,351
/ PRIOR FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: US 60/377,611
/ PRIOR FILING DATE: 2002-05-06
/ NUMBER OF SEQ ID NOS: 1140
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 372
/ LENGTH: 294
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US20040014040A1 MA851814
US-10-191-803-372

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Query Match	10.4%;	Score 178;	DB 16;	Length 294;
Best Local Similarity	100.0%;	Pred. No. 3.4e-83;		
Matches 178;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY 1075 AAATCATGAGACTGAGTGACATTTCCAAAGAAAATGCGCAAATAAAGAGATATGTTAC 1134
 Db 294 AAATCCATGAGACTGAGTGACATTTCCAAAGAAAATGCGCAAATAAAGAGATATGTTAC 235
 OY 1135 TTCCAGGCCACATCAACAATTGATAGATGAAATCTGTAAGATCAATCATCCAGGTAGCA 1194
 Db 234 TTCCAGGCCACATCAACAATTGATAGATGAAATCTGTAAGATCAATCATCCAGGTAGCA 175
 OY 1195 GATGTCCCAATCCCAACACTGACAGCCCTGACAATCACTCATGATGACTTATGTGACT 1252
 Db 174 GATGTCCCAATCCCAACACTGACAGCCCTGACAATCACTCATGATGACTTATGTGACT 117

RESULT

US-09-943-075A-7
Sequence 7, Application US/09943075A
Patent No. US70020151486A1
GENERAL INFORMATION:
APPLICANT: Popoff, Steven N.
APPLICANT: Safado, Favez F.
APPLICANT: Owen, Thomas A.
APPLICANT: Smock, Steven B.
TITLE OF INVENTION: Osteocalcin Protein and Nucleic Acids Encoding the Same,
TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
FILE REFERENCE: 71369.262
CURRENT APPLICATION NUMBER: US/09/943,075A
CURRENT FILING DATE: 2001-08-30

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; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Mouse
US-09-943-075A-7

Query Match      4.6%; Score 79; DB 9; Length 1725;
Best Local Similarity 100.0%; Pred. No. 8,2e-31;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 827 ACTGTGCACTTTCACAAAGTGAACCTTTGGGAGCAACACTGGCTCTTTTGTGTCACAA 886
 Db 827 ACTGTGCACTTTCACAAAGTGAACCTTTGGGAGCAACACTGGCTCTTTTGTGTCACAA 886
 QY 887 ATCACTTGAATCAAC 905
 Db 887 ATCACTTGAATCAAC 905

RESULT 7

```

/ Sequence 27, Application US/09623038A
/ US-09-823-038A-27
/ Patent No. US2002005835A1
/ GENERAL INFORMATION:
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Abernethy, Nevlin
/ APPLICANT: Onrust, Rene
/ APPLICANT: Kumble, Arand
/ APPLICANT: Murlison, Greg
/ TITLE OF INVENTION: Compositions Isolated From Stromal Cells
/ TITLE OF INVENTION: and Methods For Their Use
/ FILE REFERENCE: 11000.103763
/ CURRENT APPLICATION NUMBER: US/09/823.038A
/ CURRENT FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 2213
/ TYPE: DNA
/ ORGANISM: Mouse
/ US-09-823-038A-27

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Query Match	4.6%	Score 79;	DB 9;	Length 2213;
Best Local Similarity	100.0%	Pred. No. 8.2e-31;		
Matches 79;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy 827 ATCTGGCATTCTTCACAAAGTGGAACTTTGGGACAACAACCTGGCTGTGTGTCTCCACA 888
 Db 849 ACTCTGCATTCTTCACAAAGTGGAACTTTGGGACAACAACCTGGCTGTGTGTCTCCACA 908
 Qy 887 ATTCACATTGAACTACAC 905
 Db 909 ATTCACACTTGGATACAC 927

RESULT

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US-09-908-975-1458
; Sequence 1458, Application US/09908975
; Publication No. US20030165843A1
;
GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Ilat
; APPLICANT: FAIGLER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
;

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CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: Patent version 3.0
SEQ ID NO 1458
LENGTH: 65
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-908-975-1458

Query Match
Best Local Similarity 100.0%; Score 65; DB 10; Length 65;
Pred. No. 2,4e-23;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 770 GAGACCTCCCTTTCTTGATGCTGATTCAGATCCGATCCGATCTTTCTCACTACT 829
Db 1 GAGACCTCCCTTTCTTGATGCTGATTCAGATCCGATCCGATCTTTCTCACTACT 60
Qy 830 CTGCC 834
Db 61 CTGCC 65

RESULT 9
US-09-864-761-18279/c
Sequence 18279, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18279
LENGTH: 318
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005082.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 27
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: Q14956, EVALUE 8.00e-46
OTHER INFORMATION: EST HUMAN HIT: BE672596.1, EVALUE 0.00e+00
OTHER INFORMATION: NT HIT: AF322909.1, EVALUE 0.00e+00
US-09-864-761-18279

Query Match
Best Local Similarity 100.0%; Score 33; DB 9; Length 318;
Pred. No. 2e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 896 TGAATCAGCTATGCTCTCATGAACTTCA 928
Db 123 TGAATCAGCTATGCTCTCATGAACTTCA 91

RESULT 10
US-09-864-761-1520/c
Sequence 1520, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00660
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1520
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005082.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 27
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2
US-09-864-761-1520
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Query Match      1.9%; Score 33; DB 9; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      896 TGAATCACACGATGTGCTCAATGGAACCTTCA 928
DB      319 TGAATCACACGATGTGCTCAATGGAACCTTCA 287
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RESULT 11
US-10-309-290-153
; Sequence 153, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murhey, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Hailong
```

```

; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuiSeqList version 0.1
; SEQ ID NO 153
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
US-10-309-290-153
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Query Match      1.9%; Score 33; DB 17; Length 1393;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      896 TGAATCACACGATGTGCTCAATGGAACCTTCA 928
DB      840 TGAATCACACGATGTGCTCAATGGAACCTTCA 872
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RESULT 12
US-10-309-290-149
; Sequence 149, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murhey, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
```

APPLICANT: Starling, Gary
APPLICANT: Taupier, Raymond J.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/336,600
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,285
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/341,540
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/344,297
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/344,303
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/373,288
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/380,981
PRIOR FILING DATE: 2002-05-15
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 274
SOFTWARE: CuroSeqdist version 0.1
SEQ ID NO 149
LENGTH: 1410
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1410)
US-10-309-290-149

Query Match 1.9%; Score 33; DB 17; Length 1410;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 896 TGAATCACAGTATGTGCTCAATGGAACCTTCA 928
DB 830 TGAATCACAGTATGTGCTCAATGGAACCTTCA 862

RESULT 13
US-10-309-290-147
Sequence 147, Application US/10309290
Publication No. US20040023241A1
GENERAL INFORMATION:
APPLICANT: Alsebrook II, John P.
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Chiklaku, Rajeev A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Gould-Rochberg, Bonnie E.
APPLICANT: Guo, Xiaojia
APPLICANT: Jeffers, Michael E.
APPLICANT: Ji, Weizhen
APPLICANT: Li, Li
APPLICANT: Maljankar, Uriel M.
APPLICANT: Miller, Charles E.
APPLICANT: Murphy, Ryan
APPLICANT: Paturajan, Meera
APPLICANT: Peyman, John A.

APPLICANT: Raetelli, Luca
APPLICANT: Rieger, Daniel X.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Smithson, Glenda
APPLICANT: Starling, Gary
APPLICANT: Taupier, Raymond J.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/336,600
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,285
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/341,540
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/344,297
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/344,303
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/373,288
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/380,981
PRIOR FILING DATE: 2002-05-15
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 274
SOFTWARE: CuroSeqdist version 0.1
SEQ ID NO 147
LENGTH: 1542
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1542)
US-10-309-290-147

Query Match 1.9%; Score 33; DB 17; Length 1542;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 896 TGAATCACAGTATGTGCTCAATGGAACCTTCA 928
DB 830 TGAATCACAGTATGTGCTCAATGGAACCTTCA 862

RESULT 14
US-09-943-075A-8
Sequence 8, Application US/09943075A
Patent No. US2002015146A1
GENERAL INFORMATION:
APPLICANT: Popoff, Steven N.
APPLICANT: Safado, Fayer F.
APPLICANT: Owen, Thomas A.
APPLICANT: Smock, Steven L.
TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,
TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
FILE REFERENCE: 71369,262
CURRENT APPLICATION NUMBER: US/09/943,075A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/229,006
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8

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; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Human
US-09-943-075A-8

Query Match          1.9%; Score 33; DB 9; Length 1683;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      896 TGAATCACACGATATGTGCTCAATGGAACCTTCA 928
Db      896 TGAATCACACGATATGTGCTCAATGGAACCTTCA 928

RESULT 15
US-10-309-290-151
; Sequence 151, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgese, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Curation version 0.1
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; SEQ ID NO 151
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..(1774)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: wherein n may be a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: wherein n may be a, c, g or t
US-10-309-290-151

Query Match          1.9%; Score 33; DB 17; Length 1923;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      896 TGAATCACACGATATGTGCTCAATGGAACCTTCA 928
Db      990 TGAATCACACGATATGTGCTCAATGGAACCTTCA 1022

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Job time : 713 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2004, 16:15:45 ; Search time 121 Seconds

(without alignments)
2623.404 Million cell updates/sec

Title: US-09-943-075A-2

Perfect score: 572
Sequence: 1 MESLGVVFLIAGLPLQ.....PSRGRDRKPKPLQDKPMWL 572

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Ygapop 60.0, Ygapext 60.0
Pgapop 6.0, Pgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 segs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1360453

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Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-YGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTDS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	181	31.6	2303	4	US-09-197-970B-4
2	43	7.5	335	1	US-09-985-799-111
3	43	7.5	335	1	US-08-594-031-111
4	43	7.5	354	1	US-09-985-799-114
5	43	7.5	354	1	US-08-594-031-114
6	43	7.5	473	1	US-09-985-799-115
7	43	7.5	473	1	US-08-594-031-115
8	43	7.5	620	1	US-09-985-799-113
9	43	7.5	620	1	US-08-594-031-113
10	43	7.5	2213	3	US-09-983-586-27
11	36	6.3	240	1	US-09-985-799-118
12	36	6.3	240	1	US-08-594-031-118

C 13	34	5.9	190	1	US-09-985-799-95	Sequence 95, App1
C 14	34	5.9	190	1	US-08-594-031-95	Sequence 95, App1
C 15	34	5.9	217	1	US-09-985-799-112	Sequence 112, App1
C 16	34	5.9	217	1	US-08-594-031-112	Sequence 112, App1
C 17	34	5.9	223	1	US-09-985-799-116	Sequence 116, App1
C 18	34	5.9	223	1	US-08-594-031-116	Sequence 116, App1
C 19	34	5.9	260	1	US-09-985-799-119	Sequence 119, App1
C 20	34	5.9	260	1	US-08-594-031-119	Sequence 119, App1
C 21	34	5.9	262	1	US-09-985-799-93	Sequence 93, App1
C 22	34	5.9	262	1	US-08-594-031-93	Sequence 93, App1
C 23	34	5.9	286	1	US-09-985-799-121	Sequence 121, App1
C 24	34	5.9	286	1	US-08-594-031-121	Sequence 121, App1
C 25	34	5.9	335	1	US-09-985-799-92	Sequence 92, App1
C 26	34	5.9	335	1	US-08-594-031-92	Sequence 92, App1
C 27	34	5.9	335	1	US-09-985-799-96	Sequence 96, App1
C 28	34	5.9	335	1	US-09-985-799-123	Sequence 123, App1
C 29	34	5.9	335	1	US-08-594-031-92	Sequence 92, App1
C 30	34	5.9	335	1	US-08-594-031-94	Sequence 94, App1
C 31	34	5.9	335	1	US-08-594-031-96	Sequence 96, App1
C 32	34	5.9	335	1	US-08-594-031-123	Sequence 123, App1
C 33	34	5.4	224	1	US-09-985-799-122	Sequence 122, App1
C 34	31	5.4	224	1	US-08-594-031-122	Sequence 122, App1
C 35	31	5.4	231	1	US-09-985-799-120	Sequence 120, App1
C 36	31	5.4	231	1	US-08-594-031-120	Sequence 120, App1
C 37	31	5.4	247	1	US-09-985-799-117	Sequence 117, App1
C 38	31	5.4	247	1	US-08-594-031-117	Sequence 117, App1
C 39	25	4.4	270	1	US-09-985-799-109	Sequence 109, App1
C 40	25	4.4	270	1	US-08-594-031-109	Sequence 109, App1
C 41	25	4.4	309	1	US-09-985-799-106	Sequence 106, App1
C 42	25	4.4	309	1	US-08-594-031-106	Sequence 106, App1
C 43	25	4.4	524	1	US-09-985-799-105	Sequence 105, App1
C 44	25	4.4	524	1	US-08-594-031-105	Sequence 105, App1
C 45	16	2.8	2669	1	US-09-985-799-91	Sequence 91, App1

ALIGNMENTS

RESULT 1
US-09-197-970B-4
Sequence 4, Application US/09197970B
Patent No. 6664385
GENERAL INFORMATION:
APPLICANT: Michele Santicola-Nadel
Joseph V. Bonventre
Catherine A. Hession
Takamaru Ichimura
Henry Wei
Richard L. Cate

TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA

ZIP: 02142

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,970B

FILING DATE: 23-NOV. 6664385-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/018,228

FILING DATE: 24-MAY-1996

ATTORNEY/AGENT INFORMATION:
NAME: Levine, Leslie W.

REGISTRATION NUMBER: 35,245
REFERENCE/DOCKET NUMBER: A010 PCT CIP


```

; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/985,799
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 04146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELETYPE: <Unknown>
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
;
; US-09-985-799-111
;
; Alignment Scores:
; Pred. No.: 6.25e-33 Length: 335
; Score: 43.00 Matches: 43
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 7.52% Indels: 0
; DB: 1 Gaps: 0
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; US-09-943-075a-2 (1-572) x US-09-985-799-111 (1-335)
;
; QY 344 ProThrluSerThProSerProSerLeuMetProThrglyTyrlsSerMetGluLeu 363
; DB 90 CCCACATTATCAACACCTAGCCCTCTTTAATGCTACTGTTACAAATCCATGAGCTG 149
;
; QY 364 SerApIleSerAnGluAnCySArgIleAnArgTyrgIlyrPhaArgAlaThrIle 383
; DB 150 AGTGCATTTCCTCAATGAAACCTGCGAATTAACAGATATGGCTACTTCAAGACCAATC 209
;
; QY 384 ThrIleVal 386
; DB 210 ACAATGTGA 218
;
; RESULT 3
; US-08-594-031-111
; Sequence 111, Application US/08594031
; Patent No. 5783182
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; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 04146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELETYPE: <Unknown>
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
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; US-08-594-031-111
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; Alignment Scores:
; Pred. No.: 6.25e-33 Length: 335
; Score: 43.00 Matches: 43
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 7.52% Indels: 0
; DB: 1 Gaps: 0
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; US-09-943-075a-2 (1-572) x US-08-594-031-111 (1-335)
;
; QY 344 ProThrluSerThProSerProSerLeuMetProThrglyTyrlsSerMetGluLeu 363
; DB 90 CCCACATTATCAACACCTAGCCCTCTTTAATGCTACTGTTACAAATCCATGAGCTG 149
;
; QY 364 SerApIleSerAnGluAnCySArgIleAnArgTyrgIlyrPhaArgAlaThrIle 383
; DB 150 AGTGCATTTCCTCAATGAAACCTGCGAATTAACAGATATGGCTACTTCAAGACCAATC 209
;
; QY 384 ThrIleVal 386
; DB 210 ACAATGTGA 218
;
; RESULT 4
; US-09-985-799-114/C
; Sequence 114, Application US/09985799
; Patent No. RE38392
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
```

NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-985-799-114
Alignment Scores:
Pred. No.: 6.6e-33 Length: 354
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 1 Gaps: 0
US-09-943-075a-2 (1-572) x US-09-985-799-114 (1-354)
QY 344 ProThrlauserThrProserProserleuMetProThrlGlyTyrIysSerMetGluLeu 363
Db 139 CCCACATTAATACACCTACCCCTCTTAAATGCTACTGTTACAAATCATGAGAGCTG 80
QY 364 SerAspIleSerAangluAncCysArgIleAsnArgTyrGlyTyrPheArgAlaThrIle 383
Db 79 AGTGACATTTCAATGAAATCGCGATTAACAGATATGGCTACTTCAGAGCCACCATC 20
QY 384 ThrIleVal 386
Db 19 ACAATTGTA 11
RESULT 5
US-08-594-031-114/c
; Sequence 114, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-114
Alignment Scores:
Pred. No.: 6.6e-33 Length: 354
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 1 Gaps: 0
US-09-943-075a-2 (1-572) x US-08-594-031-114 (1-354)
QY 344 ProThrlauserThrProserProserleuMetProThrlGlyTyrIysSerMetGluLeu 363
Db 139 CCCACATTAATACACCTACCCCTCTTAAATGCTACTGTTACAAATCATGAGAGCTG 80
QY 364 SerAspIleSerAangluAncCysArgIleAsnArgTyrGlyTyrPheArgAlaThrIle 383
Db 79 AGTGACATTTCAATGAAATCGCGATTAACAGATATGGCTACTTCAGAGCCACCATC 20
QY 384 ThrIleVal 386
Db 19 ACAATTGTA 11
RESULT 6
US-09-985-799-115
; Sequence 115, Application US/09985799
; Patent No. RE38392
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.

STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-985-799-115
Alignment Scores:
Pred. No.: 8,76e-33 Length: 473
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
Gaps: 0
DB: 1
US-09-943-075A-2 (1-572) x US-09-985-799-115 (1-473)
QY 344 ProThriLeuSerThProSerProSerLeuMetProThriGlyTyrIlySerMetGluLeu 363
DB 218 CCCACATTAATCAACACCTAGCCCTCTTAATGCTTACGCTTAACCAATCCATGAGACTG 277
QY 364 SerAapIleSerAaGluAaGlyIleAaAaGlyTyrPheAaGlaThrIle 383
DB 278 AGTGCATTTTCCATGAATAAAGCTGCGAATTAACAGATATGCTACTTCAAGAGCCACCATC 337
QY 384 ThrIleVal 386
DB 338 ACAATTGTA 346
RESULT 7
US-08-594-031-115
Sequence 115, Application US/08594031
Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSER: BAKER & BOTTS, L.L.P.
STATE: DC

STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-115
Alignment Scores:
Pred. No.: 8,76e-33 Length: 473
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
Gaps: 0
DB: 1
US-09-943-075A-2 (1-572) x US-08-594-031-115 (1-473)
QY 344 ProThriLeuSerThProSerProSerLeuMetProThriGlyTyrIlySerMetGluLeu 363
DB 218 CCCACATTAATCAACACCTAGCCCTCTTAATGCTTACGCTTACCAATCCATGAGACTG 277
QY 364 SerAapIleSerAaGluAaGlyIleAaAaGlyTyrPheAaGlaThrIle 383
DB 278 AGTGCATTTTCCATGAATAAAGCTGCGAATTAACAGATATGCTACTTCAAGAGCCACCATC 337
QY 384 ThrIleVal 386
DB 338 ACAATTGTA 346
RESULT 8
US-09-985-799-113
Sequence 113, Application US/09985799
Patent No. RE38392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSER: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-985-799-113
Alignment Scores:
Pred. No.: 1.14e-32 Length: 620
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 1 Gaps: 0
US-09-943-075A-2 (1-572) x US-09-985-799-113 (1-620)
QY 344 ProthleuserThProserProserleuMeProthnglyTyTylysserMetGluLeu 363
Db 218 CCACATTATCAACACCTGACCCCTTTATGCTACTGCTTCAAAATCCATGAGAGCTG 277
QY 364 SerApplIeserAnGluAnGysArGlleAsnArGTYrGlyTYrPheArGAlaThrIle 383
Db 278 AGTGACATTTCATTAATAAACTGCCGATTAACAGATATGCTACTTCAGAGCCACATC 337
QY 384 ThrIleVal 386
Db 338 ACAATTGTA 346
RESULT 9
US-08-594-031-113
Sequence 113, Application US/08594031
Patent No. 5783182
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-113
Alignment Scores:
Pred. No.: 1.14e-32 Length: 620
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 1 Gaps: 0
US-09-943-075A-2 (1-572) x US-08-594-031-113 (1-620)
QY 344 ProthleuserThProserProserleuMeProthnglyTyTylysserMetGluLeu 363
Db 218 CCACATTATCAACACCTGACCCCTTTATGCTACTGCTTCAAAATCCATGAGAGCTG 277
QY 364 SerApplIeserAnGluAnGysArGlleAsnArGTYrGlyTYrPheArGAlaThrIle 383
Db 278 AGTGACATTTCATTAATAAACTGCCGATTAACAGATATGCTACTTCAGAGCCACATC 337
QY 384 ThrIleVal 386
Db 338 ACAATTGTA 346
RESULT 10
US-09-383-586-27
Sequence 27, Application US/09383586
Patent No. 6242419
GENERAL INFORMATION:
APPLICANT: Strachan, Iorna
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevin
APPLICANT: Onrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compounds isolated from stromal cells
TITLE OF INVENTION: and methods for their use
FILE REFERENCE: 11000.1037c1
CURRENT APPLICATION NUMBER: US/09/383,586
CURRENT FILING DATE: 1999-08-26

NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 27
LENGTH: 2213
TYPE: DNA
ORGANISM: Mouse
US-09-383-586-27

Alignment Scores:
Pred. No.: 3,96e-32 Length: 2213
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 3 Gaps: 0

US-09-943-075A-2 (1-572) x US-09-383-586-27 (1-2213)

Qy 344 ProthrinSerThrProSerProSerLeuMetProthrinGlyTyrIleSerMetGluLeu 363
Db 1058 CCCGATTTCACACCTAGCCCTCTTAACTGCTTACAAATTCATGAGACTG 1117

Qy 364 SerAspIleSerAsnGluAsnGlySargIleAsnArgTyrGlyTyrPheArgAlaThrIle 383
Db 1118 AGTGACATTTCCAAATGAAACTGCCGATTAACGATATGCTACTTCAGCCACCATC 1177

Qy 384 ThrIleVal 386
Db 1178 ACAATGTGA 1186

RESULT 11
US-09-985-799-118
Sequence 118, Application US/09985799
Patent No. RE38392

GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 118:
US-09-985-799-118

Alignment Scores:
Pred. No.: 2,98e-26 Length: 240
Score: 36.00 Matches: 36
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.29% Indels: 0
DB: 1 Gaps: 0

US-09-943-075A-2 (1-572) x US-09-985-799-118 (1-240)

Qy 82 LeuThySerAspSerProAlaLeuValGlySerAsnIleThrPheValAlaLeuVal 101
Db 39 CTGACGAGTACTACCCGCTCTGTTGCTTCCAAATACCTTTGTGTGAACCTGGTG 98

Qy 102 PheProArgCysGlnIleGluAspAlaAsnGlyAsnIleValTyrGlu 117
Db 99 TTCCCGATGCGCAGAGGAGATGCTAATGCGATATGCTATAG 146

RESULT 12
US-08-594-031-118
Sequence 118, Application US/08594031
Patent No. 5783182

GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:

INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-118

Alignment Scores:
Pred. No.: 2,98e-26 Length: 240
Score: 36.00 Matches: 36
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.29% Indels: 0
DB: 1 Gaps: 0

US-09-943-075A-2 (1-572) X US-08-594-031-118 (1-240)

Qy 82 LeuthSerAspSerProAlaLeuValGlySerAsnIlePhrPheValAlaSerAlaVal 101
Db 39 CTGACAGTACTCCACCGCCTTGAGTGGGTCCTCAATATCATCTTGTGTGAGCTGTG 98

Qy 102 PheProAlaGlySerGlnIleGluAspAlaAsnGlyAsnIleValTyrGln 117
Db 99 TTCCCGAGATGCCAGAGAGAGATGCTAATGCAATATCGCTATGAG 146

RESULT 13
US-09-985-799-95/c

Sequence 95, Application US/09985799
Patent No. RE38392

GENERAL INFORMATION:

APPLICANT: THOMPSON, Timothy C.

TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

NUMBER OF SEQUENCES: 175

CORRESPONDENCE ADDRESS:

ADDRESSEE: BAKER & BOTS, L.L.P.

STREET: 1299 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2400

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/985,799

FILING DATE: 06-NOV-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/594,031

FILING DATE: 30-JAN-1996

APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0110

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700

TELEFAX: 202-639-7890

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 190 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: <Unknown>

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 95:

US-09-985-799-95

Alignment Scores:

Pred. No.: 2.1e-24

Score: 34.00

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.94% Indels: 0
DB: 1 Gaps: 0

US-09-943-075A-2 (1-572) X US-09-985-799-95 (1-190)

Qy 277 SerAlaIleSerTyrIleTyrAsnPheGlyAspAsnThrGlyLeuPheValSerAsn 296
Db 179 TCTGCCATTTCTTCAAGAGGAACTTGGGCAACACTGGCCTGTGTCTCCAACTAT 120

Qy 297 HisThrLeuAsnHisThrTyrValLeuAsnGlyTyrPheAsn 310
Db 119 CAGACTTGATATCACTATATGTCTCAATGAGAACTTCAAC 78

RESULT 14
US-08-594-031-95/c

Sequence 95, Application US/08594031

Patent No. 5783182

GENERAL INFORMATION:

APPLICANT: THOMPSON, Timothy C.

TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

NUMBER OF SEQUENCES: 175

CORRESPONDENCE ADDRESS:

ADDRESSEE: BAKER & BOTS, L.L.P.

STREET: 1299 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2400

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/594,031

FILING DATE: 30-JAN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0110

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700

TELEFAX: 202-639-7890

TELEX:

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:

LENGTH: 190 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-594-031-95

Alignment Scores:

Pred. No.: 2.1e-24

Score: 34.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 5.94%

DB: 1 Gaps: 0

US-09-943-075A-2 (1-572) X US-08-594-031-95 (1-190)

QY 277 SerAlaIleSerTyrIysTyrPheAspPheGlyAspAsnThrGlyLeuPheValSerAsn 296
DB 179 TCTGCATTTCTTCAAGTGAAGTCTTGAGGACACACTGGCTGTTGTCTCCACAAAT 120
QY 297 HisThrLeuAsnHisThrTyrValLeuAsnGlyThrPheAsn 310
DB 119 CACACTTGAATCACAATTATGTCCTCAATGGAACCTTCAAC 78

QY 297 HisThrLeuAsnHisThrTyrValLeuAsnGlyThrPheAsn 310
DB 71 CACACTTGAATCACAATTATGTCCTCAATGGAACCTTCAAC 112
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Job time : 128 secs

RESULT 15

US-09-985-799-112
Sequence 112, Application US/09985799
Patent No. RE38392

GENERAL INFORMATION:

APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:

ADDRESSEE: BAKER & BOTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2400

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/985,799

FILING DATE: 06-NOV-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/594,031

FILING DATE: 30-JAN-1996

APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0110

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700

TELEFAX: 202-639-7890

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 217 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: <Unknown>

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-09-985-799-112

Alignment Scores:

Pred. No.: 2,39e-24 Length: 217

Score: 34.00 Matches: 34

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.94% Indels: 0

DB: 1 Gaps: 0

US-09-943-075a-2 (1-572) x US-09-985-799-112 (1-217)

QY 277 SerAlaIleSerTyrIysTyrPheAspPheGlyAspAsnThrGlyLeuPheValSerAsn 296
DB 11 TCTGCATTTCTTCAAGTGAAGTCTTGAGGACACACTGGCTGTTGTCTCCACAAAT 70

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2004, 17:46:50 ; Search time 577 Seconds
(without alignments)
4484.266 Million cell updates/sec

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Perfect score: 572
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Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2936184 seqs, 2261732022 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5864370

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Published Applications NA -OPM=fastat -SUFFIX=clip2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -INIT=bits -START=1 -END=1 -MATRIX=oligo
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Database: Published Applications NA:

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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2	141	24.7	631	17	US-10-404-460-129	Sequence 129, App
3	59	10.3	294	9	US-09-917-800A-139	Sequence 139, App
4	59	10.3	294	12	US-10-152-319A-122	Sequence 122, App
5	59	10.3	294	16	US-10-191-803-372	Sequence 372, App
6	43	7.5	2213	9	US-09-823-038A-27	Sequence 27, Appl
7	36	6.3	1725	9	US-09-943-075A-7	Sequence 7, Appl 1
8	21	3.7	65	10	US-09-908-975-1458	Sequence 1458, Ap
9	16	2.8	793	15	US-10-198-846-9201	Sequence 9201, Ap
10	16	2.8	1071	15	US-10-198-846-12825	Sequence 12825, A
11	16	2.8	1393	17	US-10-309-290-153	Sequence 153, App
12	16	2.8	1410	17	US-10-309-290-149	Sequence 149, App
13	16	2.8	1542	17	US-10-309-290-147	Sequence 147, App
14	16	2.8	1563	9	US-09-943-075A-8	Sequence 8, Appl 1
15	16	2.8	1923	17	US-10-309-290-151	Sequence 151, App
16	16	2.8	2661	13	US-10-463-106-1	Sequence 1, Appl 1
17	16	2.8	2661	14	US-10-039-272-1	Sequence 1, Appl 1
18	16	2.8	2665	15	US-10-084-817-169	Sequence 169, App
19	16	2.8	2669	10	US-09-525-978B-82	Sequence 82, App
20	16	2.8	2669	13	US-10-342-887-779	Sequence 779, App
21	16	2.8	2669	13	US-10-172-118-779	Sequence 779, App
22	16	2.8	2669	16	US-10-295-027-1041	Sequence 1041, Ap
23	16	2.8	2683	13	US-10-219-535-41	Sequence 41, Appl
24	16	2.8	2683	13	US-10-232-230-41	Sequence 41, Appl
25	16	2.8	2683	13	US-10-232-224-41	Sequence 41, Appl
26	16	2.8	2683	13	US-10-227-884-41	Sequence 41, Appl
27	16	2.8	2683	15	US-10-230-163-41	Sequence 41, Appl
28	16	2.8	2683	15	US-10-230-338-41	Sequence 41, Appl
29	16	2.8	2683	15	US-10-218-631-41	Sequence 41, Appl
30	16	2.8	2683	15	US-10-230-414-41	Sequence 41, Appl
31	16	2.8	2683	15	US-10-216-159A-41	Sequence 41, Appl
32	16	2.8	2683	15	US-10-218-849-41	Sequence 41, Appl
33	16	2.8	2683	15	US-10-227-873-41	Sequence 41, Appl
34	16	2.8	2683	15	US-10-227-883-41	Sequence 41, Appl
35	16	2.8	2683	15	US-10-219-076-41	Sequence 41, Appl
36	16	2.8	2683	15	US-10-230-434-41	Sequence 41, Appl
37	16	2.8	2683	15	US-10-219-003-41	Sequence 41, Appl
38	16	2.8	2683	15	US-10-219-075-41	Sequence 41, Appl
39	16	2.8	2683	15	US-10-219-466-41	Sequence 41, Appl
40	16	2.8	2683	15	US-10-219-466-41	Sequence 41, Appl
41	16	2.8	2683	15	US-10-219-479-41	Sequence 41, Appl
42	16	2.8	2683	15	US-10-219-481-41	Sequence 41, Appl
43	16	2.8	2683	15	US-10-230-260-41	Sequence 41, Appl
44	16	2.8	2683	15	US-10-232-231-41	Sequence 41, Appl
45	16	2.8	2683	15	US-10-232-233-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-943-075A-1
Sequence 1, Application US/09943075A
Patent No. US20020151486A1
GENERAL INFORMATION:
APPLICANT: Popoff, Steven N.
APPLICANT: Safado, Reyes F.
APPLICANT: Owen, Thomas A.
TITLE OF INVENTION: Osteocalcin Protein and Nucleic Acids Encoding the Same,
TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
FILE REFERENCE: 71369 265
CURRENT APPLICATION NUMBER: US/09/943, 075A
PRIOR FILING DATE: 2001-08-30
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/229, 006
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2320
TYPE: DNA
ORGANISM: Rat osteocalcin
FEATURE:

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; NAME/KEY: CDS
; LOCATION: (115) ... (1833)
US-09-943-075a-1

Alignment Scores:
Pred. No.: 0 Length: 2320
Score: 572.00 Matches: 572
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-943-075a-2 (1-572) x US-09-943-075a-1 (1-2320)

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DB 175 GCGGCCAAGCGGTTCGATGATGCTGGGCCATGAGCAAGTATCCGATCCATGAGGGAG 234

QY 41 AsnAsnGlnLeuArgGlyTyrSerSerAspGluAsnGluTyrPaspGlnGlnLeuTyrPro 60
DB 235 AACAAACAAATTAAGTCTGCTGCTCTTCAATGAAATGAAATGGATGAAACGCTATCCA 294

QY 61 ValTyrPargArgGlyGlyGlnIyArgTyrIyAspSerTyrGlyGlyIyArgValGlnAla 80
DB 295 GTGTGGAGAGAGGGGAGAGGGCAGATGGAAGGACTCTGGGAGAGGGCGCTGTGACGCA 354

QY 81 AlaLeuThrSerAspSerProAlaLeuValGlySerAsnIleThrPheValValAsnLeu 100
DB 355 GCCCTAACCAATGATTAACCGGCTGTGGTGGTTCACAAATATACCTTGTAAGAACCTG 414

QY 101 ValPheProArgCyGsglyValAspAlaAsnGlyAsnIleValTyrGluArgAsnCyS 120
DB 415 GTGTTCCCAATGCCAGAGAGAAATGCCAAGCGCAATGCTCTATGAGAGAACTGC 474

QY 121 ArgSerAspLeuGlyLeuValAsnAspProTyrValTyrAsnTyrThrGlyValAlaAsp 140
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QY 141 AspGluAspTyrPgiuAspAsnThrSerGlnGlyGlnHisLeuArgPheProAspGlyLys 160
DB 535 GATGAGACTGGAGAACCAACACAGCCAGCCAGCACTCAGGTTCCCGAGCGGAGAG 594

QY 161 ProPheProArgProHisGlyArgGlyLysTyrPasnPheValTyrValPheHisThrLeu 180
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QY 181 GlyGlnTyrPheGlnIySleuGlyGlnCySerAlaArgValSerIleAsnThrValAsn 200
DB 655 GGTCAAGTATTTTCAAAAGCTGGGTGAGTTCAGACGAGTTTCAATATTAACAGACCAAC 714

QY 201 LeuThrValGlyProGlnValMetGlnValIleValPheArgArgHisGlyArgAlaTyr 220
DB 715 TTGACAGTTGGCCCTCGAGTCAAGTGAAGTATGTTCTTTCGAAAGCAAGCGCGGCAATC 774

QY 221 IleProIleSerLysValLysAspValTyrValIleThrAspGlnIleProIlePheVal 240
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QY 241 ThrMetTyrGlnIySaAsnAspArgAsnSerSerAspGlnIleThrPheLeuArgAsnLeuPro 260
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QY 261 IlePhePheAspValLeuIleHisAspProSerHisPheLeuAsnTyrSerAlaIleSer 280
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DB 955 TACAGTGGAACTTTGGGGAACAACCTGCGCTTTTGTCTCCAAATCAACACTTGAAT 1014

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QY 341 SerProSerProThrLeuSerThrProSerProSerLeuMetProThrGlyTyrLysSer 360
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QY 361 MetGlnLeuSerAspIleSerAsnGluAsnCyArgGlyAsnArgTyrGlyTyrPheArg 380
DB 1195 ATGAGCTGAGTGAATTTCCATGATAAACTGCGAATTAACGATATGTTACTTCCAA 1254

QY 381 AlaThrIleThrIleValAspGlyIleLeuGlnValAlaAsnIleIleGlnValAlaAspVal 400
DB 1255 GCCACCATCAATGATGATGAGATCTTAAAGATCAATCAATCAAGTNGCATGTC 1314

QY 401 ProIleProThrLeuGlnProAspAsnSerLeuMetAspPheIleValThrCysLysGly 420
DB 1315 CCAATCCCAACATGACGCTGCAACTCACTGATGACTTCACTTGTGACCTCGCAAGGG 1374

QY 421 AlaThrProThrGluAlaCyThrIleIleSerAspProThrCysGlnIleAlaGlnAsn 440
DB 1375 GCCACTCCACGGAAGCTGTACGATCACTTCAACCCCACTGCGACATGCGCCGAAAC 1434

QY 441 ArgValCysSerProValAlaValAspGluLeuCySleuLeuSerValArgArgAlaPhe 460
DB 1435 AGGCTGACAGCCCGGCTGCTGATGATGCTGCTCTCTCTCTGATGAGAGAGCTTC 1494

QY 461 AsnGlySerGlyThrTyrCysValAsnPheThrLeuGlyAspAspAlaSerLeuAlaLeu 480
DB 1495 AATGGCTCGGACGCTCTGTGATTTCACTGTGGAGAGAGATGAGAGCTGGCCCTC 1554

QY 481 ThrSerAlaLeuIleSerIleProGlyLysAsnLeuGlySerProLeuArgThrValAsn 500
DB 1555 ACAAGGCTGATCTCACTCTGCAAGACCTTAAGCTCCCTCTAGAACAGTGAAAT 1614

QY 501 GlyValLeuIleSerIleGlyCysLeuAlaMetPheValThrMetValThrIleLeuLeu 520
DB 1615 GGTGCTCATCTCATATGCTGCTCGGCATGTTTGTACCATGGTATACCATCTTCTG 1674

QY 521 TyrLysLysHisLysThrTyrLysProIleGlyAsnCyThrArgAsnValValLysGly 540
DB 1675 TACAAAAACACAAAGCGTACAAAGCCATAGAAAACGACCGAAGAGCTGTCAAAGGC 1734

QY 541 LysGlyLeuSerValPheLeuSerHisAlaLysAlaProPheSerArgIyAspArgGlu 560
DB 1735 AAAGGCTGAGTGTCTTCTCAAGCCATGCAAGCCCGCTTCTCCGAGAGACCGGAGG 1794

QY 561 LysAspProLeuLeuGlnAspLysProIlePheLeu 572
DB 1795 AAGGATCACTGCTCCAGGACAAAGCATGATGCTC 1830

RESULT 2
US-10-404-460-129
; Sequence 129, Application US/10404460
; Publication No. US20040076974A1
; GENERAL INFORMATION:
; APPLICANT: PHASE-1 Molecular Toxicology, Inc.
; APPLICANT: Kier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Uma
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Liver Necrosis Predictive Genes
; FILE REFERENCE: 2874-022
; CURRENT APPLICATION NUMBER: US/10/404,460
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/369,287
; PRIOR FILING DATE: 2002-04-01

```

NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 129
LENGTH: 631
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: predictive genes for liver necrosis
NAME/KEY: misc feature
LOCATION: 2, 588, 626
OTHER INFORMATION: n = A,T,C or G
US-10-404-460-129

Alignment Scores:
Pred. No.: 1,966-136 Length: 631
Score: 141.00 Matches: 141
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.65% Indels: 0
DB: 17 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-404-460-129 (1-631)

Qy 1 MetGluSerLeuCyGlyValLeuValPheLeuLeuAlaAlaGlyLeuProLeuGln 20
Db 163 ATGAAAGTCTGCGGGGCTCTGTAATTTCTGCTGCGTCAAGACTGCCGCTCAG 222

Qy 21 AlaAlaValArgPheArgAspValLeuGlyHisGluGlnTyrProAspHisMetArgGlu 40
Db 223 GCGGCGAAGCGGTTCGATGATGCTGCGCATGAGCATGATCCGATACATAGAGGAG 282

Qy 41 AsnAsnGlnLeuArgGlyTyrSerSerAspGluAsnGlyTyrAspGlnLeuTyrPro 60
Db 283 AACAAACCAATTACGTCGCTGCTTCCAGATGAATGATGAGATGAAACGCTGATCCCA 342

Qy 61 ValTyrArgArgGlyGlyValArgTyrPheValAspSerTyrPheGlyValArgAla 80
Db 343 GTGTGAGAGAGGAGAGGAGGAGATGAGAGAGCTCTCGAGAGAGCGGTGTGAGGCA 402

Qy 81 AlaLeuThrSerAspSerProAlaLeuValGlySerAsnIleThrPheValValAsnLeu 100
Db 403 GCCCTAACGATGATTTCAACGGCTTGTGTGGTTCATATACCTTCTGATGACTG 462

Qy 101 ValPheProArgCysGlnLysGluAspAlaAsnGlyAsnIleValTyrGluArgAsnCys 120
Db 463 GTGTCCCAAGATGCGAAGAGAGATGCGCAACGGCAATATCGCTATGAGAGACTGC 522

Qy 121 ArgSerAspLeuGlnLeuAlaSerAspProTyrValTyrAsnTyrPheThrGlyValAsp 140
Db 523 AGAAGTATTTGAGGCTGCTTTCGACCGATATGCTACATGAGACACAGGAGGAGAC 582

Qy 141 Asp 141
Db 583 GAT 585

RESULT 3
US-09-917-800A-139/c
Sequence 139, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castile, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 139
LENGTH: 294
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA851814
US-09-917-800A-139

Alignment Scores:
Pred. No.: 1,416-51 Length: 294
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.31% Indels: 0
DB: 9 Gaps: 0

US-09-943-075A-2 (1-572) x US-09-917-800A-139 (1-294)

Qy 359 LysSerMetGluLeuSerAspIleSerAsnGluAsnCyArgGlyLeuArgTyrGlyTyr 378
Db 294 AATCCATGAGCGCTGAGTACATTTCCAAATGAAATGCGCAATTAACATATGATTAC 235

Qy 379 PheAlaThrIleThrIleValAspGlyIleLeuGluValAsnIleIleGlnValAla 398
Db 234 TTCAGACGACACATCATTTGATGATGATCTTGAAGTACATCATCCAGTAGGA 175

Qy 399 AspValProIleProThrLeuGlnProAspAsnSerLeuMetAspPheIleValThr 417
Db 174 GATGCCCAATCCCACTGAGCGCTGACACTGACATCTGATGACTTCAATTGACC 118

RESULT 4
US-10-152-319A-122/c
Sequence 122, Application US/10152319A
Publication No. US20040072160A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castile, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 122
LENGTH: 294
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. AA851814
US-10-152-319A-122

Alignment Scores:
Pred. No.: 1,41e-51 Length: 294
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.31% Indels: 0
DB: 12 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-152-319A-122 (1-294).

QY 359 LysSerMetGluLeuSerAspIleSerAsnGluAsnCysArgIleAsnArgTyrGlyTyr 378
DB 294 AAATCCATGAGCTGAGTGAATTCATGAACTGCGCAATTAACAGATGTGTTAC 235
QY 379 PheArgAlaThrIleThrIleValAspGlyIleLeuGluValAsnIleIleGlnValAla 398
DB 234 TTCAGAGCCACCATCACTGATGTAATCTTGAAGTCAACATCACTCCAGGTAGCA 175
QY 399 AspValProIleProThrLeuGlnProAspAsnSerLeuMetAspPheIleValThr 417
DB 174 GATGCCCAATCCCACTGACGCTGACACTCACTGATGACTTCACTTGAC 118

RESULT 5

US-10-191-803-372/C
Sequence 372, Application US/10191803
Publication No. US20040014040A1
GENERAL INFORMATION:
APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 1140
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 372
LENGTH: 294
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:

OTHER INFORMATION: Genbank Accession No. US20040014040A1 AA851814
US-10-191-803-372

Alignment Scores:
Pred. No.: 1,41e-51 Length: 294
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.31% Indels: 0
DB: 16 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-191-803-372 (1-294)

QY 359 LysSerMetGluLeuSerAspIleSerAsnGluAsnCysArgIleAsnArgTyrGlyTyr 378
DB 294 AAATCCATGAGCTGAGTGAATTCATGAACTGCGCAATTAACAGATGTGTTAC 235
QY 379 PheArgAlaThrIleThrIleValAspGlyIleLeuGluValAsnIleIleGlnValAla 398
DB 234 TTCAGAGCCACCATCACTGATGTAATCTTGAAGTCAACATCACTCCAGGTAGCA 175
QY 399 AspValProIleProThrLeuGlnProAspAsnSerLeuMetAspPheIleValThr 417
DB 174 GATGCCCAATCCCACTGACGCTGACACTCACTGATGACTTCACTTGAC 118

RESULT 6
US-09-823-038A-27
Sequence 27, Application US/09823038A
Patent No. US20020058335A1
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevin
APPLICANT: Onrust, Rene
APPLICANT: Kumble, Anand
APPLICANT: Marison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
FILE REFERENCE: 11000.103763
CURRENT APPLICATION NUMBER: US/09/823,038A
CURRENT FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 2213
TYPE: DNA
ORGANISM: Mouse
US-09-823-038A-27

Alignment Scores:
Pred. No.: 3.95e-34 Length: 2213
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 9 Gaps: 0

US-09-943-075A-2 (1-572) x US-09-823-038A-27 (1-2213)

QY 344 ProThrLeuSerThrProSerProSerLeuMetProThrGlyTyrLysSerMetGluLeu 363
DB 1058 CCACATTTACACCTACCTACCTCTTTATGCTACCTGTTACAAATCAAGAGCTG 1117
QY 364 SerAspIleSerAsnGluAsnCysArgIleAsnArgTyrGlyTyrPheArgAlaThrIle 383
DB 1118 AGTGAATTCATGAAATCGCAATTAACAGATGTGCTACTTCAAGGCCACATC 1177
QY 384 ThrIleVal 386
DB 1178 ACAATTGA 1186

RESULT 7
US-09-943-075A-7


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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12825
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1070..1071
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-12825

Alignment Scores:
Pred. No.: 2.2e-06 Length: 1071
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.80% Indels: 0
DB: 15 Gaps: 0

US-09-943-075a-2 (1-572) x US-10-198-846-12825 (1-1071)

Qy 102 PheProArgCysGlnIlySGlnAspAlaAsnGlyAsnIleValTyrGln 117
Db 459 TTCCTAGATGCCAAAAGAGATGCCAATGCCAATCATGTCTATGAG 506

RESULT 11
US-10-309-290-153
; Sequence 153, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Li, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/348,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
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; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 153
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
US-10-309-290-153

Alignment Scores:
Pred. No.: 2.82e-06 Length: 1393
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.80% Indels: 0
DB: 17 Gaps: 0

US-09-943-075a-2 (1-572) x US-10-309-290-153 (1-1393)

Qy 102 PheProArgCysGlnIlySGlnAspAlaAsnGlyAsnIleValTyrGln 117
Db 248 TTCCTAGATGCCAAAAGAGATGCCAATGCCAATCATGTCTATGAG 295

RESULT 12
US-10-309-290-149
; Sequence 149, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Li, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
```

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; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 149
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1410)
US-10-309-290-149

Alignment Scores:
Pred. No.: 2,85e-06 Length: 1410
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2,80% Indels: 0
DB: 17 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-309-290-149 (1-1410)
QY 102 PheProArgCysGlnIleGluAspAlaAsnGlyAsnIleValTyrGlu 117
DB 238 TTCCTGATGTCGCAAGAGAGATGCGCATGCGCAACATGATGCTATGAG 285

RESULT 13
US-10-309-290-147
; Sequence 147, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilkakuru, Rajeev A.
; APPLICANT: Edinger, Shommit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rochberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Patureajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rascelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
```

```

; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Wei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 147
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1542)
US-10-309-290-147

Alignment Scores:
Pred. No.: 3.1e-06 Length: 1542
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2,80% Indels: 0
DB: 17 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-309-290-147 (1-1542)
QY 102 PheProArgCysGlnIleGluAspAlaAsnGlyAsnIleValTyrGlu 117
DB 238 TTCCTGATGTCGCAAGAGAGATGCGCATGCGCAACATGATGCTATGAG 285

RESULT 14
US-09-943-075A-8
; Sequence 8, Application US/09943075A
; Patent No. US20020151486A1
; GENERAL INFORMATION:
; APPLICANT: Popoff, Steven N.
; APPLICANT: Safado, Fayer F.
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Osteocytic Protein and Nucleic Acids Encoding the Same,
; TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
; FILE REFERENCE: 71369,262
; CURRENT APPLICATION NUMBER: US/09/943,075A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1683
; TYPE: DNA
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ORGANISM: Human
US-09-943-075A-8

Alignment Scores:

Pred. No.:	3.37e-06	Length:	1683
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.80%	Indels:	0
DB:	9	Gaps:	0

US-09-943-075A-2 (1-572) x US-09-943-075A-8 (1-1683)

Qy 102 PheProArgCysGlnIysGluAspAlaAsnGlyAsnIleValTyrGlu 117
Db 304 TTCCTAGATGCCAAGAGAGATGCCAATGCGCAATATGCTATGAG 351

RESULT 15
US-10-309-290-151

Sequence 151, Application US/10309290
Publication No. US20040023241A1
GENERAL INFORMATION:

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APPLICANT: Chilikuru, Rajeev A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Gould-Rothberg, Bonnie E.
APPLICANT: Guo, Xiaojia
APPLICANT: Jeffers, Michael E.
APPLICANT: Ji, Weizhen
APPLICANT: Li, Li
APPLICANT: Malvanekar, Uriel M.
APPLICANT: Miller, Charles E.
APPLICANT: Murphy, Ryan
APPLICANT: Paturajan, Meera
APPLICANT: Peyman, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Rieger, Daniel K.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Smithson, Glenda
APPLICANT: Scaring, Gary
APPLICANT: Taupier, Raymond J.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/336,600
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,285
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/341,540
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/344,297
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/373,288
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/380,981
PRIOR FILING DATE: 2002-05-15

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 274
SOFTWARE: Cnaseqdist version 0.1
SEQ ID NO 151
LENGTH: 1923
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (95)..(1774)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: wherein n may be a, c, g or t
NAME/KEY: misc feature
LOCATION: (3)..(3)
OTHER INFORMATION: wherein n may be a, c, g or t
US-10-309-290-151

Alignment Scores:

Pred. No.:	3.82e-06	Length:	1923
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.80%	Indels:	0
DB:	17	Gaps:	0

US-09-943-075A-2 (1-572) x US-10-309-290-151 (1-1923)

Qy 102 PheProArgCysGlnIysGluAspAlaAsnGlyAsnIleValTyrGlu 117
Db 398 TTCCTAGATGCCAAGAGAGATGCCAATGCGCAATATGCTATGAG 445

Search completed: April 30, 2004, 19:21:49
Job time : 586 secs